1 G G A C A G C G T C C A A C C C		4 G G A C A G C G T C C G A C T C	PLEGGACAGCGFCCGAFCC		@ @ & O @ O O A H O O O O O O H	9 5 5 4 0 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6		NUME	1 2 3 4 5 6 7 8 9 1 1 1 1 2 1 3 1 4 5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	3102 3409 3438 3603 4052 1199 1235 1248 1265 1482 1499 1508 1509	6 7 9 3 4 0 9 3 9
G	G G G G		G G	G G		G	G G		17 18	1593 1616	
11 GGACGGCGTCCGACCTGG	12 13 G A C G G C G F C C G G C C F G G	HA 13 GGACGGCGTCTGACCTGG	OT4 LIGGACGGFGFCCGGCCFGG PLOGGACGGGGGCCFGG	PES PES GGGGAGCGTCCGACCCGG	N 1666CAGCGTCCGACCTGG	E 1 G G G C A G T G T C C G G G	16TACAACGTCTGACCTGG	9 1GTACAGCGTCCCACCTAG	O OCTACAGOGTCCGGCCTGG	PS ^b NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18	PS POSITION° 3102 3409 3438 3603 4054 4082 11998 12397 12489 12653 14899 15099 15099 155932 16165

							and and
		HA.	PLOT.	YPE	NUMB	ER	PS ^b PS
21	22	23	24	25	26	27	NUMBER POSITION ^o
G	G	Ģ	G	G	G	T	1 3102
T	T	T	${f T}$	Ţ	T	G	2 3409
A.	A	A	A	A.	G	G	3 3438
C	C	C	C	G	C	С	4 3603
A	Ā	A	G	A	A	A	5 4054
G	G	G	G	G	G	G	6 4082
C	C	C	C	C	С	Ġ	7 11998
G	G	G	G	G	G	G	8 12356
T	T	T	T	T	T	\mathbf{T}	9 12397
C	Ċ	T	C	С	С	С	10 12489
T	T	T	T	${f T}$	С	С	11 12653
G	G	G	Ġ	G	G	G	12 14824
A	A	A	A	A	A	A	13 14990
C	C	С	C	C	C	C	14 15089
C	Ċ	C	Ç	Ċ	С	С	15 15093
ċ	Ī	T	T	\mathbf{T}	С	Т	16 15529
Ğ	Ğ	Ġ	Ġ	G	G	G	17 15932
Ğ	Ğ	Ğ	Ğ	G	G	A	18 16165

^aAlleles for haplotypes are presented 5' to 3' in each column

The method of claim 1, wherein the nucleic acid sample contains the second copy of the individual's TNFRSF1A gene to identify [A method for haplotyping the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene of an individual, which comprises determining which of the TNFRSF1A haplotype pairs shown in the table immediately below defines both copies of the individual's TNFRSF1A gene, wherein the determining step comprises identifying] the phased sequence of nucleotides present at each of PS1-PS18 on the second copy [both copies] of the individual's TNFRSF1A gene,

comparing the phased sequence of the second copy to the TNFRSF1A haplotypes represented in Table 5; and

assigning to the individual, for the second copy of the individual's TNFRSF1A gene, a TNFRSF1A haplotype selected from the TNFRSF1A haplotypes represented in Table 5 which is consistent with the phased sequence of that second copy.[, and wherein each of the TNFRSF1A haplotype pairs consists of first and second haplotypes which comprise first and second sequences of polymorphisms whose positions and identities are set forth in the table immediately below:

^bPS = polymorphic site;

Position of PS within SEQ ID NO:1.]

מו אינו אינו	YPE PA:	r 15 A						PSp	P\$
12/12	22/22	2/2	22/20	12/10	2/1	22/23	2/11	NUMBER	POSITION°
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
G/G G/G	T/T	G/G	T/T	G/G	G/G	T/T	G/G	2	3409
A/A		A/A	A/A	A/A	A/A	A/A	A/A	3	3438
	A/A		C/C	C/C	C/C	c/c	C/C	4	3603
C/C	C/C	C/C		G/G	A/A	A/A	A/G	* 5	4054
G/G	A/A	A/A	A/A					5	4082
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G C/C	7	11998
c/c	C/C	C/C	C/C G/G	C/C G/G	C/C G/G	C/C G/G	G/G	8	12356
G/G	G/G	G/G T/T		T/T	T/T	T/T	T/T	9	12397
T/T	T/T		T/T	C/C	C/C	C/T	C/C	10	12489
C/C	C/C	c/c c/c	C/C	c/c	0/0	T/T	c/c	11	12653
C/C	T/T		T/C G/G	G/G	G/A	G/G	G/G	12	14824
G/G	G/G	G/G	A/G	G/A	A/A	A/A	A/A	13	14990
G/G	A/A C/C	A/A C/C	C/C	C/C	C/C	C/C	C/C	14	15089
C/C				c/c	c/c	c/c	c/c	15	15093
C/C	C/C	C/C	C/C		C/C	T/T	C/T	16	15529
T/T	T/T	C/C	T/T	T/C G/G	G/G	G/G	G/G	17	15932
G/G	G/G	G/G	G/G		G/G	G/G G/G	G/G G/G	18	16165
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/ G	7.0	10103
HAPLOT	YPE PA	IRª						PSb	PS
2/19	3/14		22/8	2/9	3/21	2/15	12/17	NUMBER .	POSITION ^c
	J/ 13								
					G/G			1	3102
G/G	G/G	G/G	G/G	G/G	G/G G/T	G/G	G/G G/G	1 2	
G/G G/T	G/G G/G	G/G G/G	G/G T/G	G/G G/G	G/T	G/G G/G	G/G	1 2 3	3102
G/G G/T A/A	G/G G/G A/A	G/G G/G A/G	G/G T/G A/A	G/G G/G A/A	G/T A/A	G/G G/G A/G	G/G G/G	1 2 3 4	3102 3409
G/G G/T A/A C/C	G/G G/G A/A C/C	G/G G/G A/G C/C	G/G T/G A/A C/C	G/G G/G A/A C/C	G/T A/A C/C	G/G G/G	G/G G/G A/G	1 2 3 4 5	3102 3409 3438 3603 4054
G/G G/T A/A C/C A/A	G/G G/G A/A C/C A/G	G/G G/G A/G C/C G/A	G/G T/G A/A C/C A/G	G/G G/G A/A	G/T A/A	G/G G/G A/G C/C	G/G G/G A/G C/C	1 2 3 4 5	3102 3409 3438 3603 4054 4082
G/G G/T A/A C/C A/A G/G	G/G G/G A/A C/C A/G G/G	G/G G/G A/G C/C G/A G/G	G/G T/G A/A C/C A/G G/G	G/G G/G A/A C/C A/G	G/T A/A C/C A/A	G/G G/G A/G C/C A/A	G/G G/G A/G C/C G/A	1 2 3 4 5 6	3102 3409 3438 3603 4054 4082 11998
G/G G/T A/A C/C A/A G/G C/C	G/G G/G A/A C/C A/G G/G C/T	G/G G/G A/G C/C G/A G/C	G/G T/G A/A C/C A/G G/G C/C	G/G G/G A/A C/C A/G G/G C/C	G/T A/A C/C A/A G/G C/C	G/G G/G A/G C/C A/A G/G	G/G G/G A/G C/C G/A G/G	1 2 3 4 5 6 7 8	3102 3409 3438 3603 4054 4082 11998 12356
G/G G/T A/A C/C A/A G/G C/C G/G	G/G G/G A/A C/C A/G G/G C/T G/G	G/G G/G A/C C/A G/G C/C G/G	G/G T/G A/A C/C A/G G/G	G/G G/G A/A C/C A/G G/G	G/T A/A C/C A/A G/G C/C G/G T/T	G/G G/G A/G C/C A/A G/G C/C	G/G G/G A/C C/C G/A G/G C/T T/T	1 2 3 4 5 6 7 8 9	3102 3409 3438 3603 4054 4082 11998 12356 12397
G/G G/T A/A C/C A/A G/G C/C G/G T/T	G/G G/G A/A C/C A/G G/G C/T G/G T/T	G/G G/G C/C G/G C/C G/G T/T	G/G T/G A/A C/C A/G G/G C/C T/T	G/G G/G A/A C/C A/G G/G C/C G/G	G/T A/A C/C A/A G/G C/C G/G	G/G G/G A/G C/C A/A G/G C/C G/G	G/G G/G A/G C/C G/A G/G C/T G/G	1 2 3 4 5 6 7 8 9 10	3102 3409 3438 3603 4054 4082 11998 12356 12397 12489
G/G G/T A/A C/C A/A G/G C/C G/G T/T C/C	G/G G/G A/A C/C A/G G/G C/T G/G	G/G G/G A/C C/A G/G C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/A	G/G G/G A/A C/C A/G G/G C/C G/G T/C	G/T A/A C/C A/A G/G C/C G/G T/T	G/G G/G A/C A/C G/C T/T	G/G G/G A/C G/A G/T G/G T/T C/C	1 2 3 4 5 6 7 8 9 10 11	3102 3409 3438 3603 4054 4082 11998 12356 12397
G/G G/T A/A C/C A/A G/C C/C G/G T/T C/C	G/G G/G A/A C/C A/G G/G C/T G/G T/T C/C	G/G G/G C/C G/G C/G T/C	G/G T/G A/A C/G G/G G/A T/T C/C	G/G G/G A/C A/C G/C G/C G/C	G/T A/A C/C A/A G/C G/G T/T C/C	G/G G/C A/G C G/F C	G/G G/G A/C C/A G/G G/T G/T C/C	1 2 3 4 5 6 7 8 9 10 11 12	3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824
G/G G/T A/A C/C A/A G/C G/G T/T C/C G/G	G/G G/G A/A C/G G/G C/T G/G T/T C/C G/G	G/G C A/G C G/T C C G/G C G/T C C C C G/T C C C C G/T C C C C C C C C C C C C C C C C C C C	G/G T/G A/A C/C A/G G/C G/A T/T C/C	G/G G/G A/C A/C G/C G/C G/C C/C	G/T A/A C/C A/A G/C G/G T/T C/C	G/G G / C A / G C G / C C / C C / C C / C C / C C / C C / C C / C C C / C C C / C C C C C C C C C C C C C C C C C C C C	G/G G/G A/C G/A G/T G/G T/T C/C	1 2 3 4 5 6 7 8 9 10 11 12 13	3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653
G/G G/T A/A C/C A/A G/C C/C G/G T/T C/C	G/G G/G A/A C/C A/G G/G C/T G/C T/T C/C	G/G G/G G/G G/G G/G G/T C/C	G/G T/G A/C A/G G/A T/C G/G T/C G/G	G/G G/G A/C A/C G/C C/C G/A C/C	G/T A/A C/A G/C G/G T/T C/T G/A C/C	G/G C A G C G T C C G A C	G/G G/G G/C G/A G/T G/C G/A C/C G/A	1 2 3 4 5 6 7 8 9 10 11 12 13 14	3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089
G/G G/T A/A C/C A/A G/C G/G T/T C/C G/G A/A	G/G G/G A/A C/G G/G C/T G/G T/T C/C G/G A/G	G/G G/G C/A G C/G T/C C/G A/C C/G T/C C/G A/C C/A	G/G T/G A/C G/C A/C G/A T/C G/G A/G	G/G G/G A/C G/C G/C G/C G/A C/C	G/T A/C A/C G/C G/T C/T G/A C/C	G	G/G G/G G/C G/G G/T G/C G/A C/C G/A	1 2 3 4 5 6 7 8 9 10 11 2 13 14 15	3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093
G/G G/T A/A C/A G/C G/G T/T CC/C G/A C/C	G/G G/G A/A C/G G/G C/T C/C G/G A/G C/C	G/G G C C G C C C C C C C C C C C C C C	G/G T/G A/C G/C G/A T/C G/G C/C A/C	G/G G/G A/C A/C G/C C/C G/A C/C	G/T A/C A/C G/C G/T C/T G/C T/C T/C	G G G C A G C G T C C G A C C C C	G/G G/G G/G G/T G/T CC/G G/C T/C	1 2 3 4 5 6 7 8 9 10 11 2 13 14 15 16	3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529
G/G G/T A/A C/A G/C G/T/C G/A C/C A/A C/C	G/G G/A C/C G/G G/T C/C G/G C/C G/C C/C	G/G C A G C G C C C G G C C C C C C C C C	G/G T/G A/C G/C G/A TC/C GA/C C/C	G/G G/G A/C G/C G/C G/C G/A C/C	G/T A/C A/C G/T/C T/C A/C C/C G/T/C G/C G/C G/C G/C	G G G C A G C G T C C G A C C C G	G/G G/G G/G G/T G/C G/C G/C G/C G/C G/C G/C G/C G/C G/C	1 2 3 4 5 6 7 8 9 1 0 1 1 2 1 3 1 4 1 5 6 1 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529 15932
G/G G/T A/A G/C G/F C/C G/A C/C T/C C/T	G/G G/A C/C G/T G/T C/C G/G T/C C/C T/T	G/G G/G C G/G C G/G G/C G/G G/G G/G G/G	G/G T/G A/C A/G G/A TC/C G/G C/C T/T	G/G G/A C/C G/C G/C C/C G/A C/C C/T	G/T A/C A/C G/C G/T C/T G/C T/C T/C	G G G C A G C G T C C G A C C C C	G/G G/G G/G G/T G/T CC/G G/C T/C	1 2 3 4 5 6 7 8 9 10 11 2 13 14 15 16	3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529

ייט זמ גע	YPE PA	TDå						PS ^b	PS
2/21	22/3	- 22 / 25 - 17	12/25	12/24	12/13	3/16	22/16	NUMBER	POSITIONG
G/G	24/3 G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
G/T	T/G	T/T	G/T	G/T	G/G	G/G	T/G	2	3409
A/A	A/A	A/A	A/A	A/A	A/A	A/G	A/G	3	3438
c/c	C/C	C/G	C/G	C/C	C/C	c/c	C/C	4	3603
A/A	A/A	A/A	G/A	G/G	G/G	A/A	A/A	5	4054
G/G	G/G	G/G	G/A G/G	G/G	G/G	G/G	G/G	6 -	4082
C/C	C/C	C/C	C/C	c/c	C/C	C/C	c/c	7	11998
	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
G/G m/m	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
C/C	C/C	c/c	c/c	c/c	c/c	d/c	c/c	10	12489
C/T	T/C	T/T	C/T	C/T	C/T	c/c	T/C	11	12653
G/G	G/G	Ġ/Ġ	G/G	G/G	G/G	G/G	G/G	12	14824
A/A	A/A	A/A	G/A	G/A	G/A	A/A	A/A	13 '	14990
c/c	C/C	Ĉ/Ĉ	c/c	C/C	c/c	c/c	c/c	14	15089
c/c	c/c	c/c	c/c	c/c	c/c	c/c	c/c	15	15093
c/c	T/T	T/T	T/T	T/T	T/T	T/T	T/T	16	15529
G/G	G/G	G/G	G/G	G/G	Ġ/Ġ	G/G	G/G	17	15932
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165
474	G/G	G/G	9/0	4/4	- C1 / C1	U , U	-, -	7.	
HAPLO'	TYPE PA	.IRª						PS ^b	PS
HAPLO' 3/27	TYPE PA 22/10	IR ^a 2/16	2/26	22/11	12/7	22/2	22/18	NUMBER	POSITION°
3/27 G/T	22/10 G/G	2/16 G/G	G/G	G/G	G/G	G/G	G/G	NUMBER 1	POSITION° 3102
3/27	22/10	2/16 G/G G/G	G/G G/T	G/G T/G	G/G G/G	G/G T/G	G/G T/T	NUMBER 1 2	POSITION° 3102 3409
3/27 G/T G/G A/G	22/10 G/G T/G A/A	2/16 G/G G/G A/G	G/G G/T A/G	G/G T/G A/A	G/G G/G A/A	G/G T/G A/A	G/G T/T A/A	NUMBER 1 2 3	POSITION° 3102 3409 3438
3/27 G/T G/G	22/10 G/G T/G A/A C/C	2/16 G/G G/G A/G C/C	G/G G/T A/G C/C	G/G T/G A/A C/C	G/G G/G A/A C/C	G/G T/G A/A C/C	G/G T/T A/A C/C	NUMBER 1 2 3	POSITION° 3102 3409 3438 3603
3/27 G/T G/G A/G	22/10 G/G T/G A/A	2/16 G/G G/G A/G	G/G G/T A/G	G/G T/G A/A C/C A/G	G/G G/G A/A C/C G/A	G/G T/G A/A C/C A/A	G/G T/T A/A C/C A/A	NUMBER 1 2 3	POSITION° 3102 3409 3438 3603 4054
3/27 G/T G/G A/G C/C	22/10 G/G T/G A/A C/C A/G G/G	2/16 G/G G/G A/G C/C A/A G/G	G/G G/T A/G C/C A/A G/G	G/G T/G A/A C/C A/G G/G	G/G G/G A/A C/C G/A G/G	G/G T/G A/A C/C A/A G/G	G/G T/T A/A C/C A/A G/A	NUMBER 1 2 3 4 5	POSITION° 3102 3409 3438 3603 4054 4082
3/27 G/T G/G A/G C/C A/A G/G C/C	22/10 G/G T/G A/A C/C A/G G/G C/C	2/16 G/G G/G A/G C/C A/A G/G C/C	G/G G/T A/G C/C A/A G/G C/C	G/G T/G A/A C/C A/G G/G C/C	G/G G/G A/A C/C G/A G/G C/C	G/G T/G A/A C/C A/A G/G C/C	G/G T/T A/A C/C A/A G/A C/C	NUMBER 1 2 3 4 5 6	POSITION° 3102 3409 3438 3603 4054 4082 11998
3/27 G/T G/G A/G C/C A/A G/G	22/10 G/G T/G A/A C/C A/G G/G C/C G/G	2/16 G/G G/G A/G C/C A/A G/G C/C	G/G G/T A/G C/C A/A G/G C/C G/G	G/G T/G A/A C/C A/G G/G C/C G/G	G/G G/G A/A C/C G/A G/G C/C G/G	G/G T/G A/A C/C A/A G/G C/C G/G	G/G T/T A/A C/C A/A G/A C/C G/G	NUMBER 1 2 3 4 5 6 7 8	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356
3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T	2/16 G/G G/G A/G C/C A/A G/G C/C G/G T/T	G/G G/T A/G C/C A/A G/C G/G T/T	G/G T/A A/A C/C A/G G/G C/C G/G T/T	G/G G/G A/A C/C G/A G/G C/C G/G	G/G T/G A/A C/C A/A G/G C/C G/G T/T	G/G T/T A/A C/C A/A G/A C/C G/G T/T	NUMBER 1 2 3 4 5 6 7 8 9	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397
3/27 G/T G/G A/G C/C A/A G/C C/C G/C T/T C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	2/16 G/G G/G A/C A/A G/C C/C G/G T/T C/C	G/G G/T G/C A/A G/C G/G T/T C/C	G/G T/A C/C A/G G/C C/C T/T C/C	G/G G/A C/C G/A G/G C/C G/G T/T	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C	G/G T/A C/A C/A G/A C/G T/C	NUMBER 1 2 3 4 5 6 7 8 9	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489
3/27 G/T G/G A/G C/C A/A G/G C/C G/G T/T	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/T C/C	2/16 G/G G/G A/C A/C A/C C/C G/C C/C	G/G G/T G/C A/A G/C G/G T/C C/C	G/G T/A C/C A/G C/C G/T C/C	G/G G/A C/C G/A G/C G/C C/C C/C	G/G T/G A/A C/C A/A G/G C/C G/G T/T C/C	G/G T/A/C A/A C/G G/T/C T/T	NUMBER 1 2 3 4 5 6 7 8 9 10	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653
3/27 G/T G/G A/G C/C A/A G/C C/C G/C T/T C/C	22/10 G/G T/G A/A C/C A/G G/G C/C G/G T/C G/G	2/16 G/G G/G A/C A/C G/C G/G T/T C/C G/G	G/G G/T G/C A/G G/C G/G T/C G/G	G/G T/A C/G G/C G/T C/C T/C G/G	G/G G/G A/C G/G G/C G/G T/C C/C G/G	G/G T/G A/A C/C A/A G/C C/C G/G T/T C/C G/G	G/G TA/CAAACG/TCT/G G/TCT/G	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824
3/27 G/G G/G A/A G/C A/A G/C G/G T/C C/C G/A	22/10 G/G T/G A/A C/C A/G C/C G/G T/C G/G A/A	2/16 G/G G/G A/C A/C C/C G/G T/C C/C G/A	G/G G/T G/C A/G C/C G/G T/C C/C G/A	G/G T/A C/G G/C G/T C/C G/A A/A	G/G G/G A/C G/G C/C G/G T/C C/C G/G	G/G T/G A/A C/C A/A G/C C/C G/G T/C G/G A/A	G/G T/ACA/ACG/G G/G G/T G/A	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990
3/27 G/G G/G A/A G/C A/A G/C G/A C/C G/A C/C	22/10 G/G T/G A/A C/C A/G G/G T/C G/G T/C G/A C/C	2/16 G/G G/G A/C A/C C/C G/A C/C G/A C/C	G/G G/T G/C A/G C/C G/T C/C G/A C/C	G/G T/A C/G G/C G/T C/C G/A C/C G/A C/C	G/G G/A C/A G/C G/C G/C C/C G/C C/C G/C	G/G T/G A/A C/C A/G C/C G/G T/T C/C G/A C/C	G/G TA/CAA/CG/TCT/GA/CG/TCT/GA/C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089
3/27 G/G G/G A/G C/A G/G T/C C/C G/A C/C	22/10 G/G T/G A/A C/C A/G G/C G/C T/C G/A C/C	2/16 G/G G/G A/C A/C G/C G/C G/C G/C G/C C/C	G/G G/T G/C A/G C/G T/C C/G A/C C/C	G/G T/ACGGC/G T/CCA/CG/T/CCGA/CGC/G	G/G G/G A/C G/G G/G T/C G/G G/C C/C G/C C/C	G/G T/G A/A C/C A/G C/C G/G T/T C/C G/A C/C	G/G TA/CAA/CG/TCT/GA/CCG/TCT/GA/CC	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093
3/27 G/G G/G A/G C/A G/C G/F C/C G/A C/C T/T	22/10 G/G T/G A/A C/C G/G T/C G/A C/C T/C	2/16 g/g g/g g/C A/C A/C G/T C/C G/A C/T	G/G G/T G/C G/G G/C G/C G/A C/C G/A C/C C/C	G/G T/A/C G/C G/T/C C A/C G/T/C C T/T G/A/C G T/T	G/G G/G A/C G/C G/C G/C G/C G/C T/T	G/G T/G A/C A/C G/C G/C T/C C/C G/A C/C T/C	G/G TA/CAA/CG/TCT/GA/CCT/T	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15089 15529
3/27 G/G G/G A/G C/A G/G T/C C/C G/A C/C	22/10 G/G T/G A/A C/C A/G G/C G/C T/C G/A C/C	2/16 G/G G/G A/C A/C G/C G/C G/C G/C G/C C/C	G/G G/T G/C A/G C/G T/C C/G A/C C/C	G/G T/ACGGC/G T/CCA/CG/T/CCGA/CGC/G	G/G G/G A/C G/G G/G T/C G/G G/C C/C G/C C/C	G/G T/G A/A C/C A/G C/C G/G T/T C/C G/A C/C	G/G TA/CAA/CG/TCT/GA/CCG/TCT/GA/CC	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	POSITION° 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093

HAPLOT	YPE PA	IRª				PSb	PS
22/12	12/5	12/3	12/2	14/6	16/4	NUMBER	POSITION ^c
G/G	G/G	G/G	G/G	G/G	G/G	1	3102
T/G	G/G	G/G	G/G	G/G	G/G	2	3409
A/A	A/A	A/A	A/A	A/A	G/A	3	3438
c/c	c/c	c/c	c/c	c/c	c/c	4	3603
A/G	G/A	G/A	G/A	G/A	A/A	5	4054
G/G	G/G	G/G	G/G	G/Ģ	G/G	6	4082
C/C	.c/c	c/c	C/C	T/C	C/C	7	11998
G/G	G/G	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/T	T/T	9	12397
c/c	·C/C	C/C	C/C	C/C	C/C	10	12489
T/C	C/C	c/c	C/C	C/C	C/C	11	12653
G/G	G/G	G/G	G/G	G/G	G/G	12	14824
A/G	G/A	G/A	G/A	G/G	A/A	13	14990
C/C	C/T	C/C	C/C	c/c	c/c	14	15089
C/C	C/C	c/c	C/C	C/C	C/T	15	15093
T/T	T/C	T/T	T/C	T/C	T/C	16	15529
G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/G	G/G	G/G	G/G	G/G	G/G	18	16165

^aHaplotype pairs are represented as 1st haplotype/2nd haplotype; with alleles of each haplotype shown 5' to 3' as 1st polymorphism/2nd polymorphism in each column; ^bPS = polymorphic site;

An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) a first nucleotide sequence which comprises a tumor necrosis factor receptor superfamily, member 1A

(TNFRSF1A) isogene encoding a TNFRSF1A polypeptide with a domain capable of binding TNFa, wherein the TNFRSF1A isogene comprises nucleotides 2920-4210, 11417-12926, and 14634-16768 of SEQ ID NO:1 except the sequence is substituted by the combination of nucleotides at polymorphic sites 1 to 13 (PS1-PS18) defined by a TNFRSF1A haplotype [is] selected from the group consisting of TNFRSF1A haplotypes

[isogenes] 1-27 shown in Table 5, wherein the nucleotide positions of PS1-PS18 in SEQ ID NO:1 and the alleles at each of PS1-PS18 for each TNFRSF1A haplotype in the group are set forth in Table 5; and the table immediately below and wherein each of the isogenes comprises the regions of SEQ ID NO:1 shown in the table immediately below and wherein each of the isogenes 1-27 is further defined by the corresponding sequence of polymorphisms whose positions and identities are set forth in the table immediately below; and

Position of PS in SEQ ID NO:1.]

P.9

					MBER	a				P\$ ^b		P\$		REGI			
	1	2	3	4 5	6	7	8	9	10	NUMBE	IR.	POSITION°	NO.	EXA	IINEDa		
	G	G	G :	g G	G	G	Ģ	G	G	1.		3102	1	2920	-4210		
	G	G	G	g G	G	G	G	G	G	2		3409	1	2920	-4210		
	A	A	Α.	A. A	A	A	A	A	A	3		3438	1	2920	-4210		
	С	Ċ		c c		C	C	C	C	4		3603	1	2920	-4210		
	Ā			A. A		Ā	G	Ġ	Ģ	5		4054	1	2920	-4210		
	G	G		G G		G	Ğ	Ğ	Ğ	6		4082	1	2920	-4210		
	č	Č				ċ	ē	ā	Ģ.	7		11998		1141	7-129:	26	
	Ģ	Ğ		GG	_	Ğ	Ā	Ğ	Ğ	é		12356			7-129		
	T	T	_	ri	_	T	Ţ	č	Ť	9		12397	- 1		7-129		
	ĉ	ĉ	_	ċċ		ċ	Ĉ	Ċ	ĉ	10		12489	1		7-129		
	C	C				C	Ç	Ċ	Ċ	11		12653	i	•	7-129	- -	
	A	G		6 6	-	G	G	G	G	12		14824	1		34-167		
		-				G	G	A	A.	13		14990	i		34-167		
	A	A				_	C	Ĉ		14		15089	1		34-167		
	C	C		Ċ I		Ċ			C				1		34-167		
	C	C	_	T C		C	C	C	C	1.5		15093			34-167		
	C	C	_	0 0	_	T	Ţ	ፗ	C	16		15529	1			· ·	
	Ģ	Ģ		G G		G	G	G	G	17		15932	1		34-167		
	G	G	G	G G	G	G	G	Ģ	G	18		16165	1	140	34-167	ρφ	
		ISC	GEN	s NU	MBET	Įā.						PS ^b	PS	SEQ	ID	REGION	
	11	ISO			MBEI	^{≀ª} L5	16	17	18	19	20	PS ^b NUMBER	PS POSITION		ID	REGION EXAMINED ^d	
		. 12	2 1	3 1	.4 :		16 G	17 G	18 G	19 .G	20 G			N° ⊓		EXAMINED	
	G	12 G	2 l G	3 I	4 :	L5 3				.G		NUMBER 1	POSITION	N° 1 1 2	NO.	EXAMINED ^d 210	
1	G G	12 G G	2 1 G G	3 1 0	.4 : 1 (L5	G	Ģ	G	,	G	NUMBER 1 2	POSITION 3102	N° 1 1 2 1 2	NO. 2920-4	EXAMINED ^d 210 210	
ı	G G A	12 G G A	2 l G G A	3 1 0 0 2	.4 .	L5 3 3	6 6	G	G T	.G T	G T	NUMBER 1	POSITION 3102 3409	N° 1 1 2 1 2 1 2	NO. 2920-4 2920-4	EXAMINED ^d 210 210 210	
ı	G G A C	12 G G A C	2 1 G G A	3 1 0 0 2 7	.4 : 0	L5 3 3	9990	0000	G T A	.G T A	G T A	NUMBER 1 2 3	POSITION 3102 3409 3438	N° 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1	NO. 2920-4 2920-4 2920-4	EXAMINED ^d 210 210 210 210 210	
ı	G G A C G	12 G G A C G	2 1 G G A C	3 1 0 7 0	.4 .	L5 3 3 3 2 4	G G C A	GGGCA	G T A C A	.G T A C A	G T A C A	NUMBER 1 2 3 4 5	POSITION 3102 3409 3438 3603	N° 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1	NO. 2920-4 2920-4 2920-4 2920-4	EXAMINED ^d 210 210 210 210 210 210	
ı	GGACGG	G G A C G	2 1 G G A C G	3 1 0 7 0	.4 : 6 : 6 : 6 : 6 : 6 : 6 : 6 : 6 : 6 :	L5 3 3 3 4 4	G G C A G	GGGCAG	G T A C A	.G T A C A G	G T A C A G	NUMBER 1 2 3 4 5	POSITION 3102 3409 3438 3603 4054	N° 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1	NO. 2920-4 2920-4 2920-4 2920-4 2920-4	EXAMINED ^d 210 210 210 210 210 210 210	
ı	GGACGGC	G A C G C	2 1 G G A C G G	3 1 0 0 2 0 0	.4 : 6 : 6 : 6 : 6 : 6 : 6 : 6 : 6 : 6 :	15 5 6 7 7	G G G C A G C	OGGCAGT	G T A C A C	G T A C A G C	G T A C A G C	NUMBER 1 2 3 4 5 6 7	POSITION 3102 3409 3438 3603 4054 4082 11998	N° 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1	NO. 2920-4 2920-4 2920-4 2920-4 2920-4	EXAMINED ^d 210 210 210 210 210 210 210 12926	
	GGACGGGG	G A C G C G	2 1 G G A C G G	3 1 0 0 2 0 0	.4 : G G G G G G G G G G G G G G G G G G	15 5 5 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	GGGCAGCG	GGGCAGTG	G T A C A A C G	GTACAGGG	GFACAGOG	NUMBER 1 2 3 4 5 6 7	POSITION 3102 3409 3438 3603 4054 4082 11998 12356	N° 1 2 2 1 2 1 2 1 2 1 1 1 1 1 1 1 1 1 1	NO. 2920-4 2920-4 2920-4 2920-4 2920-4 11417-	EXAMINED ^d 210 210 210 210 210 210 12926 12926	
1	GGACGGCGF	12 GGACGGCGT	2 1 G G G G G G	3 13 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	.4 : .4 : .4 : .4 : .4 : .4 : .4 : .4 :	15 5 5 6 7 4 7 7 7 8 8	0 0 0 0 A 0 0 0 F	GGGCAGTGT	GTACAACGT	GTACAGOGT	GFACAGOGF	NUMBER 1 2 3 4 5 6 7 8	POSITION 3102 3409 3438 3603 4054 4082 11998 12356 12397	N° 11 2 2 1 2 1 2 1 1 1 1 1 1 1 1 1 1 1 1	NO. 2920-4 2920-4 2920-4 2920-4 2920-4 11417-	EXAMINED ^d 210 210 210 210 210 210 12926 12926 12926	
	GGACGGCGFC	12 GGACGGCGFC	2 1 G G G G G G G G G G G G G G G G G G	3 13 00 00 00 00 00 00 00 00 00 00 00 00 00	.4	L5	GGGCAGCGFC	0 0 0 0 A 0 F 0 F 0	GHACAACGHO	GTACAGCGTC	GTACAGCGTC	NUMBER 1 2 3 4 5 6 7 8 9	POSITION 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489	N° 1 2 2 1 2 1 2 1 1 1 1 1 1 1 1 1 1 1 1	NO. 2920-4 2920-4 2920-4 2920-4 2920-4 11417- 11417-	EXAMINED ^d 210 210 210 210 210 210 210 12926 12926 12926 12926	
	GGAUGGUGHUU	12 GGACGGCGFCC	2 I G G G G G G G G G G G G G G G G G G	3 3 3 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	.4	L	0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 A 0 H 0 H 0 O	GTACAACGTCT	GTACAGCGTCC	GFACAGCGFCC	NUMBER 1 2 3 4 5 6 7 8 9 10	POSITION 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653	N° 1 2 2 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1	NO. 2920-4 2920-4 2920-4 2920-4 2920-4 11417- 11417- 11417-	EXAMINED ^d 210 210 210 210 210 210 210 12926 12926 12926 12926 12926	
	004000000000	126640666666666	2 1 G G G G G G G G G G G G G G G G G G	3 3 3 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	.4 : : : : : : : : : : : : : : : : : : :		0000 A 0 0 0 0 0 0 0	0 0 0 0 A 0 H 0 H 0 0 0	GHACAACGHCHG	GTACAGCGTCCG	GFACAGCGFCCG	NUMBER 1 2 3 4 5 6 7 8 9 10 11	POSITION 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824	N° 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	NO. 2920-4 2920-4 2920-4 2920-4 2920-4 11417- 11417- 11417- 11417-	EXAMINED ^d 210 210 210 210 210 210 210 12926 12926 12926 12926 12926	
1	GGACGGCGFCCGA		2 1 G G G G G G G G G G G G G G G G G G	3 13 00 00 00 00 00 00 00 00 00 00 00 00 00			0 0 0 0 A 0 0 0 0 F 0 0 0 A	OGGCAGHGHCCGA	GHACAACGFCFGA	GTACAGOGTOOGA	0 F A C A G C G F C C G G	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12	POSITION 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990	N° 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	NO. 2920-4 2920-4 2920-4 2920-4 2920-4 11417- 11417- 11417- 11417- 14634-	EXAMINED ^d 210 210 210 210 210 210 210 12926 12926 12926 12926 12926 12926 16768	
	G G A U G G C G F C C G A C	1266406666660	2 1 G G G G G G G G G G G G G G G G G G	3 13 00 00 00 00 00 00 00 00 00 00 00 00 00			0 0 0 0 A 0 0 0 F 0 0 0 A 0	GGGCAGTGTCCGAC	GHACAACGHOHGAC	GTACAGCGTCCGAC	G F A C A G C G F C C C C C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13	POSITION 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089	N° 1 2 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	NO. 2920-4 2920-4 2920-4 2920-4 2920-4 11417- 11417- 11417- 114634- 14634-	EXAMINED ^d 210 210 210 210 210 210 210 12926 12926 12926 12926 12926 16768 16768 16768	
	G G A C G G C G G C C G A C C	1994099999009900	2 1 G G G G G G G G G G G G G G G G G G	3			0000A000H000A00	0 0 0 0 A 0 T 0 T 0 0 0 A 0 0	GHACAACGHCHGACC	G T A C A G C G T C C G A C C	@ F & C & B C B B C C B B C C B B C B C B C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14	POSITION 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093	N° 1 2 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	NO. 2920-4 2920-4 2920-4 2920-4 11417- 11417- 11417- 114634- 14634- 14634-	EXAMINED ^d 210 210 210 210 210 210 210 12926 12926 12926 12926 12926 16768 16768 16768	
	GGACGGCGFCCGACCF	126640660640066004	2 I G G G G G G G G G G G G G G G G G G	3			0000A00GH000A00F	0 0 0 0 A 0 T 0 F 0 0 0 A 0 0 0	GHACAACGHCHGACCH	G T A C A G C G T C C G A C C T	GFACAGCGFCCGGCCF	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	POSITION 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15093 15529	N° 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	NO. 2920-4 2920-4 2920-4 2920-4 2920-4 11417- 11417- 11417- 114634- 14634- 14634- 14634-	EXAMINED ^d 210 210 210 210 210 210 210 12926 12926 12926 12926 12926 16768 16768 16768 16768	
	G G A C G G C G G C C G A C C	1994099999009900	2 1 G G G G G G G G G G G G G G G G G G	3			0000A000H000A00	0 0 0 0 A 0 T 0 T 0 0 0 A 0 0	GHACAACGHCHGACC	G T A C A G C G T C C G A C C	@ F & C & B C B B C C B B C C B B C B C B C	NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14	POSITION 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093	N° 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	NO. 2920-4 2920-4 2920-4 2920-4 11417- 11417- 11417- 114634- 14634- 14634-	EXAMINED ^d 210 210 210 210 210 210 210 12926 12926 12926 12926 12926 16768 16768 16768 16768	

P.10



	ISOG	ENE	NUMB	ERª		PS ¹	.	PS	SEQ ID	REGION
21	22	23	24	25	26	27	NUMBER	POSITION	v° NO.	EXAMINED
G	G	G	G	G	G	T	1	3102	1.	2920-4210
T	${f T}$	${f T}$	${f T}$	${f T}$	Т	Ģ	2	3409	1	2920-4210
A	A	A	A	A	G	G	3	3438	1	2920-4210
C	С	C	С	G	C	Ç	4	3603	1	2920-4210
A	A	A	G	A	A	A	5	4054	1	2920-4210
G	G	G	G	G	G	G	6	4082	1	2920-4210
С	C	C	Ç	¢	C	С	7	11998	1	11417-12926
G	G	G	G	G	G	G	8	12356	1	11417-12926
T	T.	Т	T	T	T	T	9	12397	1	11417-12926
Ĉ	C	T	С	C	C	¢	10	12489	1.	11417-12926
T	T	T	T	T	Ċ	C	11	12653	1	11417-12926
G	G	G	Ġ	Ģ	G	G	12	14824	1	14634-16768
A	A	A	A	A	A	A	13	14990	1	14634-16768
C	С	C	C	C	C	C	14	15089	1	14634-16768
Ċ	ā	Ċ	Ċ	C	C	С	15	15093	1	14634-16768
Ċ	Ť	Ţ	Ť	T	С	T	16	15529	1	14634-16768
G	G	G	G	G	Ģ	G	17	15932	1	14634-16768
Ġ	Ğ.	G	Ğ	Ğ	Ğ	A	1.8	16165	1	14634-16768

^{*}Alleles for isogenes are presented 5' to 3' in each column;

(b) a second nucleotide sequence which is complementary to the first nucleotide sequence.

24. An isolated fragment of a tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) isogene, wherein the fragment comprises at least 15 [10] nucleotides in one of the regions of SEQ ID NO:1 selected from nucleotides 2920-4210, 11417-12926, or 14634-16768 [shown in the table immediately below] and wherein the fragment comprises one or more polymorphisms selected from the group consisting of thymine at PS1, guanine at PS4, adenine at PS12, thymine at PS14, thymine at PS15, adenine at PS17 and adenine at PS18, wherein the nucleotide positions in SEQ ID NO:1 of the [selected] polymorphisms are 3102 for PS1. 3603 for PS4, 14824 for PS12, 15089 for PS14, 15093 for PS15, 15932 for PS17 and 16165 for PS18. [has the position set forth in the table immediately below:

^bPS = polymorphic site;

Position of PS in SEQ ID NO:1;

^dRegion examined represents the nucleotide positions defining the start and stop positions within SEQ ID NO:1 of the sequenced region.]

LOGACAGCOFCCAACCCGG	266404606100640006	GOGHCCGACHC	5 G G	N6 GGACAGCGTCCGGCCCGG	® © © A O © © O A H O O © © O O H ©	900ACGGCGCCCCACCFGG	100A00000H000A00000	PS*NUMBE 1 2 3 4 5 .6 7 8 9 10 11 12 13 14 15 16 17 18		PS POSITIONS 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15529 15529 155229 16165	SEQ ID NO. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	REGION EXAMINE 2920-42 2920-42 2920-42 2920-42 11417-1 11417-1 11417-1 11417-1 114634-1 14634-1 14634-1 14634-1 14634-1	210 210 210 210 210 22926 22926 22926 22926 26768 26768 26768
11 GGACGGCGTCCGACCTGG	2 106ACGGCGFCCGGCCFGG	ISOG ACGGCGTCTGACCTGG	E14 E1GGACGGTGFCCGGCCFGG	NUS 1000CAGCGTCCGACCCGG	R ² 6 BE 1 G G G C A G C G T C C G A C C T G G		8 16 1 4 C 4 4 C 6 T C T G 4 C C T G 6	16 TACAGCGTCCGACCTAG	O	PS ^b NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18	PS POSITION 3102 3409 3438 3603 4054 4082 11998 12356 12397 12489 12653 14899 15093 155932 16165		REGION EXAMINED ⁴ 2920-4210 2920-4210 2920-4210 2920-4210 2920-4210 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 11417-12926 114634-16768 114634-16768 114634-16768 114634-16768

		ISOG	ENE	NUME	BER		PS ^b	PS	SEQ ID	REGION
21	22	23	24	25	26	27	NUMBER	POSITION	NO.	EXAMINED
G	G	G	G	G	G	Ţ	1	3102	1.	2920-4210
T	T	T	\mathbf{T}	T	T	G	2	3409	1	2920-4210
A	A	A	A	A	G	G	3	3438	1	2920-4210
C .	C	С	Ç	G	¢	С	4	3603	1	2920-4210
A	A	A.	G	A	A	A	5	4054	1	2920-4210
G	G	G	G	G	G	G	6	4082	1	2920-4210
C	Ç	¢	Ċ	C	C	C	7	11998	1	11417-12926
G-	G	G	G	G ·	G	G	8	12356	1	11417-12926
T	T	T	Ŧ	T	T	T	9	12397	1	11417-12926
C	С	T	C	C	C	C	10	12489	1	11417-12926
T	T	T	${f T}$	T	C	¢	11	12653	1	11417-12926
Ġ	G	G	G	G	G	G	12	14824	1	14634-16768
A	A	A	A	A	A	A	13	14990	1	14634-16768
Ç	С	Ç	C	С	Ċ	C	14	15089	1,	14634-16768
С	C	С	C	Ç	¢	C	15	15093	1	14634-16768
Ç	T	Т	Т	ጧ	¢	Ţ	16	15529	1,	14634-16768
G	G	G	G	G	G	G	17	15932	1	14634-16768
G	G	G	G	G	Ģ	A	18	16165	1	14634-16768

^{*}Alleles for isogenes are presented 5' to 3' in each column;

25. An isolated polynucleotide comprising a TNFRSF1A coding sequence, [wherein the coding sequence is selected from the group consisting of 8, 9, 14, 17, and 19 shown in the table immediately below, and] wherein [each of] the coding sequence comprises SEQ ID NO:2, except for being substituted with an adenine at position 935.[at each of the polymorphic sites which have the positions in SEQ ID NO:2 and polymorphisms set forth in the table immediately below:

Isog	ene	Coding	Sequence	Number	PS	PS
8 _	9	14,17	19		Number	Position
a	C	T	С		7	224
A	G	G	G		8	362
T	Ċ	T	T		9	403
G	G	G	A		17	935

^aAlleles for the isogene coding sequence are presented 5' to 3' in each column; the numerical portion of the isogene coding sequence number represents the number of the parent full TNFRSF1A isogene;

Please cancel claim 33.

Please add the following new claims:

^bPS = polymorphic site;

Position of PS in SEQ ID NO:1;

^dRegion examined represents the nucleotide positions defining the start and stop positions within SEQ ID NO:1 of the sequenced region.]

^bPS = polymorphic site; *Position of PS in SEQ ID NO:2.]

- 35. The isolated polynucleotide of claim 20, wherein the isogene encodes a TNFRSF1A polypeptide identical to SEQ ID NO:3 and wherein the isogene is selected from the group consisting of isogenes 1,2,3,4,5,6,7,10,11,12,13,15,16,18,20, 21,22, 23,24,25,26 and 27.
- 36. The isolated polynucleotide of claim 20, wherein the isogene is isogene 19, encoding a TNFRSF1A polypeptide identical to SEQ ID NO:3 except for having a lysine at amino acid position 312.
- 37. The isolated polynucleotide of claim 20, wherein the isogene is isogene 8 and encodes a TNFRSF1A polypeptide identical to SEQ ID NO:3 except for having a glutamine at amino acid position 121.
- 38. The isolated polynucleotide of claim 20, wherein the isogene 9 and encodes a TNFRSF1A polypeptide identical to SEQ ID NO:3 except for having a histidine at amino acid position 135.
- 39. The isolated polynucleotide of claim 20, wherein the isogene is selected from isogenes 14 and 17 and encodes a TNFRSF1A polypeptide identical to SEQ ID NO:3 except for having a leucine at amino acid position 75.

A clean version of the amended claims is attached hereto.